

SEQUENCE LISTING

<110> Seoul National University Industry Foundation

<120> Method for stimulating wound healing

<130> OP03-1017

<150> KR 2002-42858

<151> 2002-07-22

<160> 7

<170> KopatentIn 1.71

<210> 1

<211> 312

<212> PRT

<213> Homo sapiens

<400> 1

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1 5 10 15

Glu Ala Asp Gln Ile Ile Glu Tyr Leu Lys Gln Gln Val Ser Leu Leu

20 25 30

Lys Glu Lys Ala Ile Leu Gln Ala Thr Leu Arg Glu Glu Lys Lys Leu

35 40 45

Arg Val Glu Asn Ala Lys Leu Lys Lys Glu Ile Glu Glu Leu Lys Gln

50 55 60

Glu Leu Ile Gln Ala Glu Ile Gln Asn Gly Val Lys Gln Ile Ala Phe

65 70 75 80

Pro Ser Gly Thr Pro Leu His Ala Asn Ser Met Val Ser Glu Asn Val
85 90 95

Ile Gln Ser Thr Ala Val Thr Thr Val Ser Ser Gly Thr Lys Glu Gln
100 105 110

Ile Lys Gly Gly Thr Gly Asp Glu Lys Lys Ala Lys Glu Lys Ile Glu
115 120 125

Lys Lys Gly Glu Lys Lys Glu Lys Lys Gln Gln Ser Ile Ala Gly Ser
130 135 140

Ala Asp Ser Lys Pro Ile Asp Val Ser Arg Leu Asp Leu Arg Ile Gly
145 150 155 160

Cys Ile Ile Thr Ala Arg Lys His Pro Asp Ala Asp Ser Leu Tyr Val
165 170 175

Glu Glu Val Asp Val Gly Glu Ile Ala Pro Arg Thr Val Val Ser Gly
180 185 190

Leu Val Asn His Val Pro Leu Glu Gln Met Gln Asn Arg Met Val Ile
195 200 205

Leu Leu Cys Asn Leu Lys Pro Ala Lys Met Arg Gly Val Leu Ser Gln
210 215 220

Ala Met Val Met Cys Ala Ser Ser Pro Glu Lys Ile Glu Ile Leu Ala
225 230 235 240

Pro Pro Asn Gly Ser Val Pro Gly Asp Arg Ile Thr Phe Asp Ala Phe
245 250 255

Pro Gly Glu Pro Asp Lys Glu Leu Asn Pro Lys Lys Lys Ile Trp Glu
260 265 270

Gln Ile Gln Pro Asp Leu His Thr Asn Asp Glu Cys Val Ala Thr Tyr
275 280 285

Lys Gly Val Pro Phe Glu Val Lys Gly Lys Gly Val Cys Arg Ala Gln
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Thr Met Ser Asn Ser Gly Ile Lys
305 310

<210> 2
<211> 108
<212> DNA
<213> Artificial Sequence

<220>
<223> probe for Southern blot

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gcgcagctgt gctcgacgtt gtcactgaag cggaaggac tggctgct 108

<210> 3
<211> 1226
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<213> Artificial Sequence

<220>
<223> probe for Southern blot

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aatgtgtgtg tgcctgcatt tgtgtgtatg caccattgcg tgcataccta gagcctgcag	180
aggctagaag aggggttcaa cctggaactg aggctacagg tggttgtga gtatccacat	240
agatgctcgg aattaaacct gggttctcca gtcccaagga gactaaatai ttcaaagta	300
agcctgcact ttgtactaca gtaaaataaa accactgtgg agtgactaat ataaaatagt	360
aagatgagct ctgattaac aggcaaaagt ttaagtttct agtattgta aagtagcacc	420
atctccctaa agagaaccat atttatttct ctccagtct tctgtgttct cctctttgt	480
ttgaaagtt agtgagtgt tttttctct actgtgaaca caacatgaga caaactcagg	540
gattgtaaga gatcatggac ataaattact tttaggaacc tggcactcaa algaaaatta	600
attagigaca agttggcatg gcattttatt attaacctg ggtggnnnnn nnnnnnnnn	660
nnntaaactg cgtgggtgatg atttgtgatt gcaagaagac atagatatga agctctgaac	720
aacagtgtcc aggcaacatg tgaagaaaag gccctatgga ggggcaggag agcaggtgag	780
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tgtaaagtgt tcttcaccta aggtttgtg actgtaacca cttttctaa agaaaacatt	900
aagaaaaaca tagglgtctg ttgccttct atttgtgtg gtgattaaaa cgctgaccaa	960
aagcaactg gctgaggagc cgttttgtta ttctccgtt taggtagcaa lgaagtigga	1020
gcaggaggaa ggggtcttac aggctagctc tctgcctc cttgagcaag cattctgtg	1080
gtagctcagg actccctgca cagtgcaca ccacgtgctt cttcaggggg acttcaaact	1140

actgtacacc ctttccttct gtcgaccata tgggagagct cccaacgcgt tggatgcata 1200

gcttgagtat tnnnnnnnnn nagctt 1226

<210> 4
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> IF3 primer for PCR

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<210> 5
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> IR3 primer for PCR

<400> 5
cgttacttaa gctagcttgc cacctac 27

<210> 6
<211> 31
<212> DNA
<213> Artificial Sequence

<220>

<223> pKOF2 primer for PCR

<400> 6

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31

<210> 7

<211> 838

<212> DNA

<213> Artificial Sequence

<220>

<223> p43-specific probe for Northern blot

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caggttgctc ttcttaagga gaaagcaatt ttgcaggcaa caatgagaga agaaaagaaa 180

cttcgagttg aaaatgctaa actgaaaaa gaaatagaag agctaaagca agagctgatt 240

ctggcagaaa ttcataacgg agtggagcaa gtgcgtgttc gattgaglac tccactgcag 300

acgaactgta ctgcttctga aagtgtgggt cagtctccat cagtagcaac caccgcctct 360

ccigctacaa aagagcagat caaagcggga gaagaaaaga aggtgaaaga gaagactgaa 420

aagaaaggag agaaaaagga gaagcagcag tcggcagcag caagtactga ctccaagcct 480

atcgacgcat cgcgtctgga tcttcgaatt ggttgtattg ttactgcaa gaagcaccct 540

gatgcagatt cactgtatgt ggaggaagta gatgtgggag aagcagcccc gcgcacggtc	600
gtcagcgggc tggatgaalca tgttcctcta gaacagatgc aaaalcgtat ggtggtttta	660
ctctgtaatc tgaagcctgc aaagatgcgg ggagttctgt ctcaagccat ggtgatgtgt	720
gccagttcac cagagaaagt ggagattctg gccctccca acgggtccgt tctggggac	780
agaattactt ttgatgcltt tctgggagag cctgacaagg agctaaacc taagaaga	838

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